

SCORE Search Results Details for Application 10573229 and Search Result 20090528_121056_us-10-573-229a-1.rge.

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This page gives you Search Results detail for the Application 10573229 and Search Result 20090528_121056_us-10-573-229a-1.rge.

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OM nucleic - nucleic search, using sw model

Run on: May 31, 2009, 21:47:12 ; Search time 916 Seconds
(without alignments)
101538.085 Million cell updates/sec

Title: US-10-573-229A-1
Perfect score: 920
Sequence: 1 tctgtagagggaatggctg.....acccccaaagaaaccttcta 920

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 14594359 seqs, 50548307366 residues

Total number of hits satisfying chosen parameters: 29188718

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
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6: gb_rod:*
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 12: gb_inv:*
 13: gb_mam:*
 14: gb_bct:*
 15: gb_htgl:*
 16: gb_htg2:*
 17: gb_htg3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description	
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	1	920	100.0	920	2	CS074575	CS074575 Sequence
	2	920	100.0	920	2	CS430220	CS430220 Sequence
	3	920	100.0	920	2	DJ044325	DJ044325 Identific
c	4	422.2	45.9	109238	5	AL133538	AL133538 Human DNA
	5	306	33.3	308	5	Z79429	Z79429 H.sapiens f
c	6	275	29.9	140243	15	AC067760	AC067760 Homo sapi
c	7	275	29.9	147659	15	AC015496	AC015496 Homo sapi
c	8	275	29.9	172212	5	AL136100	AL136100 Human DNA
	9	226.8	24.7	186029	16	AC169795	AC169795 Macaca mu
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c	12	176.6	19.2	390	2	CS430486	CS430486 Sequence
	13	122.6	13.3	561	2	AR612609	AR612609 Sequence
	14	122.6	13.3	561	2	AR799123	AR799123 Sequence
	15	122.6	13.3	561	2	DD052947	DD052947 SINGLE CO
	16	121.2	13.2	541	2	AR612608	AR612608 Sequence
	17	121.2	13.2	541	2	AR799122	AR799122 Sequence
	18	121.2	13.2	541	2	DD052946	DD052946 SINGLE CO
c	19	120	13.0	124409	5	AC069360	AC069360 Homo sapi
	20	120	13.0	165031	5	AC023850	AC023850 Homo sapi
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	25	109.6	11.9	180602	5	AC010873	AC010873 Homo sapi
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c	29	108	11.7	201170	15	AC022259	AC022259 Homo sapi
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	31	105	11.4	117916	17	AC225094	AC225094 Loxodonta
	32	105	11.4	123795	17	AC218085	AC218085 Loxodonta
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	34	104.8	11.4	737	2	EA735231	EA735231 Sequence
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c	40	103.4	11.2	176644	5	AP002982	AP002982 Homo sapi
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	43	103.2	11.2	206939	16	AC174979	AC174979 Bos tauru
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ALIGNMENTS

RESULT 1

CS074575

LOCUS CS074575 920 bp DNA linear PAT 05-MAY-2005

DEFINITION Sequence 1 from Patent WO2005030250.

ACCESSION CS074575

VERSION CS074575.1 GI:63091182

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Tuereci, O., Sahin, U., Helftenbein, G. and Schlueter, V.

TITLE Identification of tumour-associated cell surface antigens for diagnosis and therapy

JOURNAL Patent: WO 2005030250-A 1 07-APR-2005;

Ganymed Pharmaceuticals AG (DE)

FEATURES

source Location/Qualifiers
 1. .920
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 920; DB 2; Length 920;

Best Local Similarity 100.0%; Pred. No. 7.4e-275;

Matches 920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG	60

Qy	61	CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC	120
Db	61	CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC	120
Qy	121	TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC	180
Db	121	TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC	180
Qy	181	AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT	240
Db	181	AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT	240
Qy	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGACCTCCATCAGGTGTCGACAAGGAA	300
Db	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGACCTCCATCAGGTGTCGACAAGGAA	300
Qy	301	GATCCCAGTAGGGCAGGAGACAGGAGCACCTCTGCTGTGGCCAATGCAGGAATGCTGGCC	360
Db	301	GATCCCAGTAGGGCAGGAGACAGGAGCACCTCTGCTGTGGCCAATGCAGGAATGCTGGCC	360
Qy	361	ATCATTGCTTCTGCTGGGCGACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTACG	420
Db	361	ATCATTGCTTCTGCTGGGCGACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTACG	420
Qy	421	TGGAGTGAAAACCTTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAA	480
Db	421	TGGAGTGAAAACCTTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAA	480
Qy	481	TTTCTCTGCTTCTGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTA	540
Db	481	TTTCTCTGCTTCTGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTA	540
Qy	541	AAACCTCCTCTGCCCCAGGCCCAAGCAAGGATTTCCTAGCGGGGAGGAAGGTAGAATC	600
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Qy	661	CAACACAAGGGAAGTACCTGCTGGGTTCTGGGGTTGGGGAAGGAAAATCCCTACTGCCC	720
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Qy	721	CAAGAGCCAGCCCCGAACCAAGGCACAGCTTATACTGGCCCCGGGGCCTGGGGGGGCAC	780
Db	721	CAAGAGCCAGCCCCGAACCAAGGCACAGCTTATACTGGCCCCGGGGCCTGGGGGGGCAC	780
Qy	781	GAAAACCTTGAAAAAGGGGCGCCTTCCCAGCTTCCCCGGGGTAAGGGCTTTACCCCCCA	840
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Qy 841 GAGGGGGGGGAAAAATCCGAGTGGGATCTTTCCCAACCGCCGAAGACTAAAACCTTTAA 900
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 Db 841 GAGGGGGGGGAAAAATCCGAGTGGGATCTTTCCCAACCGCCGAAGACTAAAACCTTTAA 900
 Qy 901 ACCCCCAAAGAAACCTTCTA 920
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 Db 901 ACCCCCAAAGAAACCTTCTA 920

RESULT 2

CS430220

LOCUS CS430220 920 bp DNA linear PAT 19-OCT-2006

DEFINITION Sequence 1 from Patent WO2006100089.

ACCESSION CS430220

VERSION CS430220.1 GI:116291601

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE

1
 AUTHORS Sahin,U., Tuereci,O., Koslowski,M., Helftenbein,G., Usener,D. and
 Schlueter,V.

TITLE Identification of surface-associated antigens for tumor diagnosis
 and therapy

JOURNAL Patent: WO 2006100089-A 1 28-SEP-2006;
 Ganymed Pharmaceuticals AG (DE)

FEATURES Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 920; DB 2; Length 920;
 Best Local Similarity 100.0%; Pred. No. 7.4e-275;
 Matches 920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCAGTGGAGAGGTG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCAGTGGAGAGGTG 60
 Qy 61 CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC 120
 Qy 121 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db	121	TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC	180
Qy	181	AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT	240
Db	181	AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT	240
Qy	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGACCTCCATCAGGTGTCGACAAGGAA	300
Db	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGACCTCCATCAGGTGTCGACAAGGAA	300
Qy	301	GATCCAGTAGGGCAGGAGACAGGAGCACCTCTGCTGTGGCCAATGCAGGAATGCTGGCC	360
Db	301	GATCCAGTAGGGCAGGAGACAGGAGCACCTCTGCTGTGGCCAATGCAGGAATGCTGGCC	360
Qy	361	ATCATTGCTTCTGCTGGGCGACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTACG	420
Db	361	ATCATTGCTTCTGCTGGGCGACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTACG	420
Qy	421	TGGAGTGAAAACCTTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAA	480
Db	421	TGGAGTGAAAACCTTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAA	480
Qy	481	TTTCTCTGCTTCTGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTA	540
Db	481	TTTCTCTGCTTCTGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTA	540
Qy	541	AAACCTTCCCTGCCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATC	600
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Qy	601	GAGAGACCTCTAACCTTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAA	660
Db	601	GAGAGACCTCTAACCTTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAA	660
Qy	661	CAACACAAGGAAGTACCTGCTGGGTTCTGGGGGTGGGGAAGGAAAATCCCTACTGCCC	720
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Qy	721	CAAGAGCCAGCCCCGAACCAAGGCACAGCTTATACTGGCCCCGGGGCCTGGGGGGGCAC	780
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Qy	781	GAAAACCTTGAAAAAGGGGCGCCTTCCCAGCTTCCCCGGGGGTAAAGGCTTTACCCCCCA	840
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Qy	841	GAGGGGGGGGAAAAATCCGAGTGGGATCTTTCCCAACCGCCGAAGACTAAACCTTTAA	900
Db	841	GAGGGGGGGGAAAAATCCGAGTGGGATCTTTCCCAACCGCCGAAGACTAAACCTTTAA	900
Qy	901	ACCCCCAAAGAAACCTTCTA	920

Db 901 ACCCCCAAAGAAACCTTCTA 920

RESULT 3

DJ044325

LOCUS DJ044325 920 bp DNA linear PAT 26-OCT-2007

DEFINITION Identification of Tumour-Associated Cell Surface Antigens for
Diagnosis and Therapy.

ACCESSION DJ044325

VERSION DJ044325.1 GI:158737401

KEYWORDS JP 2007506417-A/1.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 920)

AUTHORS Herufutembain,G., Shuryuta,V., Sahin,U. and Tureci,O.

TITLE Identification of Tumour-Associated Cell Surface Antigens for
Diagnosis and TherapyJOURNAL Patent: JP 2007506417-A 1 22-MAR-2007;
Ganymed Pharmaceuticals AGCOMMENT OS Homo sapiens
PN JP 2007506417-A/1
PD 22-MAR-2007
PF 23-SEP-2004 JP 2006527354
PR 26-SEP-2003 DE 10344799.7
PI geert herufutembain,volker shuryuta,ugur sahin,oezlem tureci
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FH Key Location/Qualifiers.FEATURES Location/Qualifiers
source 1. .920
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN

Query Match 100.0%; Score 920; DB 2; Length 920;
Best Local Similarity 100.0%; Pred. No. 7.4e-275;
Matches 920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 60
 Db 1 TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 60

Qy 61 CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC 120
 Db 61 CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC 120

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Db	121	TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC	180
Qy	181	AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT	240
Db	181	AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT	240
Qy	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGACCTCCATCAGGTGTCGACAAGGAA	300
Db	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGACCTCCATCAGGTGTCGACAAGGAA	300
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Db	301	GATCCAGTAGGGCAGGAGACAGGAGCACCTCTGCTGTGGCCAATGCAGGAATGCTGGCC	360
Qy	361	ATCATTGCTTCTGCTGGGCGACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTACG	420
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Qy	421	TGGAGTGAAAACCTTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAA	480
Db	421	TGGAGTGAAAACCTTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAA	480
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Db	601	GAGAGACCTCTAACCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAA	660
Qy	661	CAACACAAGGGAAGTACCTGCTGGGTTCTGGGGTTGGGGAAGGAAAATCCCTACTGCCC	720
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Qy	721	CAAGAGCCAGCCCCGAACCAAGGCACAGCTTATACTGGCCCCGGGGCCTGGGGGGGCAC	780
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Qy	781	GAAAACCTTGAAAAAGGGGCGCCTTCCCAGCTTCCCCGGGGTAAGGGCTTTACCCCCCA	840
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Qy 901 ACCCCCAAAGAAACCTTCTA 920
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 Db 901 ACCCCCAAAGAAACCTTCTA 920

RESULT 4

AL133538/c
 LOCUS AL133538 109238 bp DNA linear PRI 07-MAY-2008

DEFINITION Human DNA sequence from clone RP11-550N16 on chromosome 6q26-27
 Contains a CpG island, complete sequence.

ACCESSION AL133538

VERSION AL133538.16 GI:12666199

KEYWORDS HTG; CpG island.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 109238)

AUTHORS Wallis, J.

TITLE Direct Submission

JOURNAL Submitted (30-APR-2008) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
 Clone requests: Geneservice (<http://www.geneservice.co.uk/>) and
 BACPAC Resources (<http://bacpac.chori.org/>)

COMMENT On Feb 5, 2001 this sequence version replaced gi:12655232.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: vega@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one subclone; and the assembly was confirmed by restriction digest,
 except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
 on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep

This sequence was generated from part of bacterial clone contigs of
 human chromosome 6, constructed by the Sanger Centre Chromosome 6
 Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr6>

RP11-550N16 is from the library RPCI-11.2 constructed by the group

of Pieter de Jong. For further details see
<http://bacpac.chori.org/>
 VECTOR: pBACe3.6.

FEATURES	Location/Qualifiers
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ORIGIN

Query Match 45.9%; Score 422.2; DB 5; Length 109238;
Best Local Similarity 94.5%; Pred. No. 3.1e-119;
Matches 460; Conservative 0; Mismatches 23; Indels 4; Gaps 2;

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QY	377	GGCGACTGAGAAGCATACCCACTTCCCCAGAACCTTTTTTACGTGGAGTGAAAACCTTTA	436
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QY	437	AGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAATTCTCTGCTTCTGCA	496
Db	95942	AGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAATTCTCTGCTTCTGCA	95883
QY	497	AAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTAAAACCTCCCTGCCCC	556
Db	95882	AAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTAAAACCTCCCTGCCCC	95823
QY	557	AGGCCCCAAGCAAGGATTTCCTAGCGGGGAGGAAGGTAGAATCGAGAGACCTCTAACCC	616
Db	95822	AGGCCCCAAGCAAGGATTTCCTAGCGGGGAGGAAGGTAGAATCGAGAGACCTCTAACCC	95763
QY	617	TGGGAGAGGAGGGAGGGAAAATCTCCGAGGACCAGGGTTATGCAACAACACAAGGGAAGTA	676
Db	95762	TGGGAGAGGAGGGAGGGAAAATCTCCGAGGACCAGGGTTATGCAACAACACAAGGGAAGTA	95703
QY	677	CCTGCTGGGTTCTGGGGGTTGGGGAAGGAAAATCCCTACTGCCCAAGAGCCAGCCCCGA	736
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 Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
 Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.

TITLE Direct Submission

JOURNAL Submitted (27-APR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT On Sep 23, 2000 this sequence version replaced gi:7651809.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L9986

Center clone name: 309_K_2

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 128933 bases at least Q40

Consensus quality: 134958 bases at least Q30

Consensus quality: 136879 bases at least Q20

Insert size: 148000; agarose-fp

Insert size: 137643; sum-of-contigs

Quality coverage: 3.5 in Q20 bases; agarose-fp

Quality coverage: 3.8 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 27 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 4248: contig of 4248 bp in length

* 4249 4348: gap of 100 bp

* 4349 5605: contig of 1257 bp in length

* 5606 5705: gap of 100 bp

* 5706 7181: contig of 1476 bp in length

* 7182 7281: gap of 100 bp

* 7282 9012: contig of 1731 bp in length

* 9013 9112: gap of 100 bp

```

*      9113      10509: contig of 1397 bp in length
*      10510     10609: gap of 100 bp
*      10610     13120: contig of 2511 bp in length
*      13121     13220: gap of 100 bp
*      13221     15323: contig of 2103 bp in length
*      15324     15423: gap of 100 bp
*      15424     17407: contig of 1984 bp in length
*      17408     17507: gap of 100 bp
*      17508     20878: contig of 3371 bp in length
*      20879     20978: gap of 100 bp
*      20979     22666: contig of 1688 bp in length
*      22667     22766: gap of 100 bp
*      22767     26227: contig of 3461 bp in length
*      26228     26327: gap of 100 bp
*      26328     29552: contig of 3225 bp in length
*      29553     29652: gap of 100 bp
*      29653     33144: contig of 3492 bp in length
*      33145     33244: gap of 100 bp
*      33245     35959: contig of 2715 bp in length
*      35960     36059: gap of 100 bp
*      36060     40873: contig of 4814 bp in length
*      40874     40973: gap of 100 bp
*      40974     46108: contig of 5135 bp in length
*      46109     46208: gap of 100 bp
*      46209     50453: contig of 4245 bp in length
*      50454     50553: gap of 100 bp
*      50554     54780: contig of 4227 bp in length
*      54781     54880: gap of 100 bp
*      54881     60935: contig of 6055 bp in length
*      60936     61035: gap of 100 bp
*      61036     68604: contig of 7569 bp in length
*      68605     68704: gap of 100 bp
*      68705     75243: contig of 6539 bp in length
*      75244     75343: gap of 100 bp
*      75344     81214: contig of 5871 bp in length
*      81215     81314: gap of 100 bp
*      81315     87663: contig of 6349 bp in length
*      87664     87763: gap of 100 bp
*      87764     94389: contig of 6626 bp in length
*      94390     94489: gap of 100 bp
*      94490     105834: contig of 11345 bp in length
*      105835     105934: gap of 100 bp
*      105935     125401: contig of 19467 bp in length
*      125402     125501: gap of 100 bp
*      125502     140243: contig of 14742 bp in length.

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Query Match 29.9%; Score 275; DB 15; Length 140243;
 Best Local Similarity 100.0%; Pred. No. 2.7e-73;
 Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 60
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Qy      61 CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC 120
          |||
Db      51728 CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC 51669

Qy      121 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180
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Db      51668 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 51609

Qy      181 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240
          |||
Db      51608 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 51549

Qy      241 GTCCTTGATTCTTAACCCACAGAAATTGTGTAAG 275
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Db      51548 GTCCTTGATTCTTAACCCACAGAAATTGTGTAAG 51514

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RESULT 7
 AC015496/c
 LOCUS AC015496 147659 bp DNA linear HTG 16-MAR-2000
 DEFINITION Homo sapiens clone RP11-21E5, WORKING DRAFT SEQUENCE, 7 unordered
 pieces.
 ACCESSION AC015496

VERSION AC015496.3 GI:7249030
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 147659)
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 TITLE Homo sapiens, clone RP11-21E5
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 147659)
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
 Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
 Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
 Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
 Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
 Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
 Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
 Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
 McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
 Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
 Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
 Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
 Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 COMMENT On Mar 16, 2000 this sequence version replaced gi:6553986.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L3993
 Center clone name: 21_E_5
 ----- Summary Statistics
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 129300 bases at least Q40
 Consensus quality: 140951 bases at least Q30
 Consensus quality: 145175 bases at least Q20
 Insert size: 146000; agarose-fp
 Insert size: 147059; sum-of-contigs

Quality coverage: 5.8 in Q20 bases; agarose-fp

Quality coverage: 5.7 in Q20 bases; sum-of-contigs

-----.

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 7 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 2851: contig of 2851 bp in length
 * 2852 2951: gap of 100 bp
 * 2952 6911: contig of 3960 bp in length
 * 6912 7011: gap of 100 bp
 * 7012 13475: contig of 6464 bp in length
 * 13476 13575: gap of 100 bp
 * 13576 29402: contig of 15827 bp in length
 * 29403 29502: gap of 100 bp
 * 29503 54805: contig of 25303 bp in length
 * 54806 54905: gap of 100 bp
 * 54906 87698: contig of 32793 bp in length
 * 87699 87798: gap of 100 bp
 * 87799 147659: contig of 59861 bp in length.

FEATURES	Location/Qualifiers
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gap	2852. .2951 /estimated_length=100
misc_feature	2952. .6911 /note="assembly_fragment; clone_end:T7; vector_side:right"
gap	6912. .7011 /estimated_length=100
misc_feature	7012. .13475 /note="assembly_fragment"
gap	13476. .13575 /estimated_length=100
misc_feature	13576. .29402 /note="assembly_fragment"
gap	29403. .29502 /estimated_length=100
misc_feature	29503. .54805 /note="assembly_fragment"

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gap          54806. .54905
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              /estimated_length=100
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              /note="assembly_fragment;
              clone_end:SP6;
              vector_side:right"

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ORIGIN

Query Match 29.9%; Score 275; DB 15; Length 147659;
 Best Local Similarity 100.0%; Pred. No. 2.8e-73;
 Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 60
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Db          41178 TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 41119

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Qy          121 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180
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Qy          181 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240
              |||
Db          40998 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 40939

Qy          241 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAG 275
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RESULT 8

AL136100/c

LOCUS AL136100 172212 bp DNA linear PRI 06-MAY-2008

DEFINITION Human DNA sequence from clone RP11-534P19 on chromosome 6 Contains
 a pseudogene similar to zinc finger proteins, complete sequence.

ACCESSION AL136100

VERSION AL136100.12 GI:11322762

KEYWORDS HTG; zinc finger.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 172212)

AUTHORS Bird,C.

TITLE Direct Submission

JOURNAL Submitted (30-APR-2008) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
Clone requests: Geneservice (<http://www.geneservice.co.uk/>) and BACPAC Resources (<http://bacpac.chori.org/>)

COMMENT On Nov 23, 2000 this sequence version replaced gi:11139882.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: vega@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6>
RP11-534P19 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://bacpac.chori.org/>
VECTOR: pBACe3.6.

FEATURES

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.8e-73;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTTG 60
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Qy      121 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180
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Qy      181 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240
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Db 93144 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 93085

Qy      241 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAG 275
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Db 93084 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAG 93050

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RESULT 9

AC169795

LOCUS AC169795 186029 bp DNA linear HTG 12-NOV-2005

DEFINITION Macaca mulatta clone CH250-283M17, WORKING DRAFT SEQUENCE, 3 ordered pieces.

ACCESSION AC169795

VERSION AC169795.2 GI:82174563

KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE Macaca mulatta (rhesus monkey)

ORGANISM Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.

REFERENCE 1 (bases 1 to 186029)

AUTHORS

Muzny,D.M., Abraham,K.K., Abulimiti,A., Adams,C.Q., Aduba,G., Allen,C.C., Alsbrooks,S.L., Anosike,U.S., Archer,P.M., Arredondo,H.H., Attaway,T., Bandaranaike,D.P., Bangura,L., Barton,S.R., Bell,A.V., Bell,S.N., Beraducci,A.R., Bickham,C., Biswal,K., Blyth,P.R., Buhay,C.J., Canada,A., Cardenas,V.,

Carter,K., Chacko,J., Chandrabose,M.N., Chavez,A., Chavez,D.,
 Chen,G., Chen,R., Chu,H., Clerc blankenburg,K.P., Cockrell,R.,
 Cooper,J.A., Coyle,M.D., Cree,A., Cueto,C.B., Curry,S.M., Dai,W.,
 Dao,M.D., Davila,M., Davis,C., Davy-Carroll,L., Del fierro,P.,
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 Dugan-Rocha,S., Dunn,A.M., Durbin,K.J., Ebong,V.E., Egan,A.,
 Espinosa,V.C., Fa,M., Fernandez,S., Fernando,P.R., Ferrer,A.R.,
 Flagg,N., Forbes,L.D., Fowler,R.G., Fu,Q., Fuh,E., Gabisi,R.A.,
 Ganardhanan,M., Ganer,J., Garcia iii,R.M., Garcia,A.M.,
 Garcia,S.M., Garner,T.T., Ghose,S., Gingras,M.,
 Gonzalez-Garay,M.L., Guevara,W.V., Haaland,W.C., Haeberlen,K.A.,
 Hagans,B.J., Hall,O., Hamid,H., Hamilton,K.A., Hampton,O.A.,
 Harbes,B.A., Harris,R.A., Havlak,P., Hawes,A.C., Hawkins,E.S.,
 Haynes,S.J., Hemphill,L., Hernandez,J., Hines,S., Hirani,K.,
 Hitchens,M.E., Hodgson,A.V., Hagues,M.E., Holder,M., Hollins,B.,
 Howell,L.L., Hulyk,S.W., Hume,J., Jackson,A., Jackson,L.R.,
 Jacob,S.K., Jhangiani,S.N., Jiang,H., Johnson,B., Johnson,R.,
 Joshi,V., Joy,C., Kaikai,F.B., Kalafus,K.J., Kalu,J.B., Kang,Y.,
 Keebler,J., Khan,Z.M., Kidwai,S., King,L.M., Kisamo,H., Kovar,C.L.,
 Kowis,A.N., Kowis,C.R., Lago,L.A., Lago,M.T., Lai,C., Lara,F.,
 Le,T.T., Lee,S.L., Lee,T.W., Legall iii,F.H., Lemon,S.J.,
 Lewis,L.R., Li,B., Li,Y., Li,Z., Linnell,M.A., Liu,J., Liu,W.,
 Liu,Y., Liu,Y., Liyanage,D., London,P., Lopez,J., Lorensuhewa,L.M.,
 Lozado,R.J., Luc,T., Madu,R.C., Maheshwari,M., Maheshwari,R.,
 Malloy,K., Mansouri,D.L., Martinez,E., Matejkova,P., Mathew,T.,
 Mccauley,S.K., Mcpherson,J.D., Mercado,C., Mercado,I.C.,
 Metzker,M.L., Millin,A., Milosavljevic,A., Morgan,M.B., Morris,S.,
 Mundayasa,M., Murray,D.D., Muzny,D.M., Nazareth,L.V., Ngo,D.N.,
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 Richards,S., Rojas,A., Ruiz,S., Sabo,A., Santibanez,J.,
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 Trejos,Z.Y., Usmani,K., Vargo,C.E., Vattathil,S., Vega,R.A.,
 Villasana,D., Volkov,A., Walker,D.L., Wang,Q., Wang,S.,
 Warren,J.T., Watt,J.E., Wei,X., Wheeler,D.A., White,C.S., Williams
 jr,R.L., Williams,A.C., Williams,G.A., Williams,J.D., Wilson,K.,
 Woodworth,J.R., Worley,K.C., Wright,R.A., Wu,J., Wu,W., Yakub,S.,
 Yerrapragada,S., Yu,F., Yuan,D.T., Yuan,Y., Zhang,J., Zhang,L.,
 Zhang,Z., Zhou,J., Zhu,Y., Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 186029)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (12-OCT-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 186029)

AUTHORS Worley, K.C.

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COMMENT On Nov 12, 2005 this sequence version replaced gi:77539482.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help.tmc.edu

----- Project Information

Center project name: LDVL

Center clone name: CH250-283M17

----- Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye: 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 186011 bases at least Q40

Consensus quality: 186345 bases at least Q30

Consensus quality: 186634 bases at least Q20

Estimated insert size: 205029; sum-of-contigs estimation

Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* The sequence data in this record represents an 'enhanced' version

* of a Phase 2 submission. The indicated order and orientation of

* each sequence has been established using one or more of the

* following: read-pair data from individual subclones, overlaps

* with neighboring clones, alignment with available reference

* sequence (e.g., human), and/or confirmation by PCR testing.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 54276: contig of 54276 bp in length

* 54277 54376: gap of 100 bp

* 54377 104140: contig of 49764 bp in length

* 104141 104340: gap of 200 bp

* 104341 186029: contig of 81689 bp in length.

http://es.ScoreAccessWeb/GetItem.action?AppId=105732...8_121056_us-10-573-229a-1.rge&ItemType=4&startByte=0 (24 of 31) 6/15/2009 10:35:40 AM

http://es.ScoreAccessWeb/GetItem.action?AppId=105732...8_121056_us-10-573-229a-1.rge&ItemType=4&startByte=0 (27 of 31) 6/15/2009 10:35:40 AM

http://es.ScoreAccessWeb/GetItem.action?AppId=105732...8 121056 us-10-573-229a-1.rge&ItemType=4&startByte=0 (28 of 31)6/15/2009 10:35:40 AM

ORIGIN

Query Match 13.3%; Score 122.6; DB 2; Length 561;
Best Local Similarity 69.6%; Pred. No. 4.7e-26;
Matches 201; Conservative 0; Mismatches 74; Indels 14; Gaps 2;

Qy	2	CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCACTGGAGAGGTTGC	61
Db	201	CTCTGGGGGAAGCCAGCTGCCATGTCATGAGGACACTCAAGCAGCCCTGTGGAGAGGGCCC	260
Qy	62	ACTTGGTGAGAAACCGATGCCT-CTGCCAACCACTGCACTAACCTGCTGGGTC-----	114
Db	261	ATGTGGCAAGGAAGCTGAGGCCTCCTGCCAACAGCCAGCAAGGAAGCTGAGGCCTCCTGCCA	320
Qy	115	-----TGAGACTGAGCCACTTTGGAAGTGATCTTGGAGCACCAGTCAAGCCCTTAGC	167
Db	321	ACAGCCATGTGAGTGAGCCATCTTGAAGCAGATCCTCCAGCCCCAGTCAAGCCTTCAGA	380
Qy	168	TGGCTGCAGCCACAGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATC	227
Db	381	TGACTGCAGCCCCAGCTAACATCTTGACTGCAACCTCATGAGAGACCCTGAGCCAGAACC	440
Qy	228	CCCTGGCTAAATTTGCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA	276
Db	441	ACCCAGCTTAAGCTGCTCCTAAATTCCTGACCCACAGAAACTGTGAGAGA	489

RESULT 15

DD052947

LOCUS DD052947 561 bp DNA linear PAT 04-NOV-2005

DEFINITION SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING SAME.

ACCESSION DD052947

VERSION DD052947.1 GI:92688538

KEYWORDS JP 2004523201-A/108.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

Job time : 957 secs

SCORE 3.0